Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claim 1 (currently amended): A method for identifying a transcribed region of interest of a genome comprising:

a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and

b) Identifying said transcribed region as a region of said genome where the hybridization intensities of all consecutive probes targeting said region are above a threshold value.

Claim 2 (original): The method of claim 1 wherein said probes are oligonucleotides.

Claim 3 (currently amended): The method of ~~claim 3~~ claim 2 wherein said oligonucleotides are immobilized on a substrate.

Claim 4 (original): The method of claim 1 wherein said threshold is non-specific binding.

.1   Claim 5 (previously presented): The method of claim 1
2   wherein said non-specific binding is measured using a probe
·3   containing at least one mismatched base.

1   Claim 6 (currently amended): The method of claim 1 further
2   comprising:
3
4   c)   Identifying a sub-region wherein said hybridization
5   intensities of said probes targeting said sub-region ~~is~~ are
6   similar, thereby indicating said sub-region as said
7   transcribed region.

1   Claim 7 (original): The method of claim 6 wherein said
2   genome is from a prokaryote.

1   Claim 8 (original): The method of claim 7 wherein said
2   transcribed region is an operon.

1   Claim 9 (previously presented): The method of claim 7
2   wherein said prokaryote is bacteria.

Claims 10-14 (canceled)